

SEQUENCE LISTING

<110> Croteau, Rodney B
Burke, Charles C

<120> GERANYL DIPHOSPHATE SYNTHASE LARGE SUBUNIT, AND METHODS
OF USE

<130> WSUR1117920

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<150> 09/420,211

<151> 1999-10-18

<150> PCT/US98/21772

<151> 1998-10-15

<150> 08/951,924

<151> 1997-10-16

<160> 15

<170> PatentIn Ver. 2.0

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<211> 1131

<212> DNA

<213> Mentha piperita

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<222> (1)..(1131)

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gtt aaa gat gtt cac ggc ggc cgg agg cgg aga tcc aga tcc act ctc	96
Val Lys Asp Val His Gly Gly Arg Arg Arg Ser Arg Ser Thr Leu	
20 25 30	
ttt caa tcc cat cca ctt cgc act gaa atg cct ttc tct ctc tac ttc	144
Phe Gln Ser His Pro Leu Arg Thr Glu Met Pro Phe Ser Leu Tyr Phe	
35 40 45	
tca tcc ccc ctc aaa gct ccc gcc act ttt tcc gtt tct gca gtt tat	192
Ser Ser Pro Leu Lys Ala Pro Ala Thr Phe Ser Val Ser Ala Val Tyr	
50 55 60	
acc aaa gag ggc agc gaa att agg gat aaa gat ccg gcg cct tcg act	240
Thr Lys Glu Gly Ser Glu Ile Arg Asp Lys Asp Pro Ala Pro Ser Thr	
65 70 75 80	
tcg ccg gcg ttc gat ttc gac gga tac atg ctc cgg aag gcg aaa tcc	288
Ser Pro Ala Phe Asp Phe Asp Gly Tyr Met Leu Arg Lys Ala Lys Ser	
85 90 95	
gtc aac aag gcg ttg gaa gcg gcg gtg cag atg aag gag ccg ctg aag	336

11317920

Val	Asn	Lys	Ala	Leu	Glu	Ala	Ala	Val	Gln	Met	Lys	Glu	Pro	Leu	Lys	
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Ile	His	Glu	Ser	Met	Arg	Tyr	tcc	Leu	Leu	Ala	Gly	125	Lys	Arg	Val	
		115					120									
cgt	cct	atg	ctg	tgc	atc	cgc	gcc	tgc	gag	ctc	gta	ggc	ggc	gac	gag	432
Arg	Pro	Met	Leu	Cys	Ile	Ala	Ala	Cys	Glu	Leu	Val	140	Gly	Gly	Asp	
		130				135										
tcc	acg	gcg	atg	ccg	gcg	gcc	tgc	gcc	gtc	gag	atg	atc	cac	acg	atg	480
Ser	Thr	Ala	Met	Pro	Ala	Ala	Cys	Ala	Val	Glu	Met	Ile	His	Thr	Met	
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tcg	ctg	atg	cac	gac	gac	ctc	cca	tgc	atg	gac	aac	gac	gac	ctc	cgc	528
Ser	Leu	Met	His	Asp	Asp	Leu	Pro	Cys	Met	Asp	Asn	Asp	Asp	Leu	Arg	
				165					170					175		
cgc	ggc	aag	ccg	acg	aac	cac	atg	gct	ttc	ggc	gag	agc	gtg	gcg	gtc	576
Arg	Gly	Lys	Pro	Thr	Asn	His	Met	Ala	Phe	Gly	Glu	Ser	Val	Ala	Val	
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ctc	gcc	ggc	gac	gcc	ctc	ctc	tcc	ttc	gcg	ttc	gag	cac	gtg	gcg	gcg	624
Leu	Ala	Gly	Asp	Ala	Leu	Leu	Ser	Phe	Ala	Phe	Glu	His	Val	Ala	Ala	
		195					200					205				
gcg	acc	aaa	ggc	gcg	ccg	ccg	gag	cgg	atc	gtg	agg	gtc	ctc	ggc	gag	672
Ala	Thr	Lys	Gly	Ala	Pro	Pro	Glu	Arg	Ile	Val	Arg	Val	Leu	Gly	Glu	
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ctg	gct	gtc	tcg	atc	ggg	tcg	gag	ggg	ctg	gtg	gcg	ggg	cag	gtg	gtg	720
Leu	Ala	Val	Ser	Ile	Gly	Ser	Glu	Gly	Leu	Val	Ala	Gly	Gln	Val	Val	
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gac	gtc	tgc	tcg	gag	ggg	atg	gcg	gag	gtc	ggg	ctg	gac	cac	ctc	gag	768
Asp	Val	Cys	Ser	Glu	Gly	Met	Ala	Glu	Val	Gly	Leu	Asp	His	Leu	Glu	
				245					250					255		
ttc	atc	cac	cac	cac	aag	acg	gcg	gcg	ctg	ctg	cag	ggg	tcg	gtg	gtt	816
Phe	Ile	His	His	His	Lys	Thr	Ala	Ala	Leu	Leu	Gln	Gly	Ser	Val	Val	
			260				265						270			
ctg	ggg	gcg	att	ttg	ggc	ggc	gga	aag	gag	gag	gag	gtg	gcg	aag	ctg	864
Leu	Gly	Ala	Ile	Leu	Gly	Gly	Gly	Lys	Glu	Glu	Glu	Val	Ala	Lys	Leu	
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aga	aaa	ttc	gcg	aat	tgc	atc	gga	ttg	ctg	ttt	cag	gtg	gtg	gac	gat	912
Arg	Lys	Phe	Ala	Asn	Cys	Ile	Gly	Leu	Leu	Phe	Gln	Val	Val	Asp	Asp	
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Ile	Leu	Asp	Val													

340	345	350	
cag ctc ctc cat ttt cat cct cat agg gca gct cca ttg att gct ctc			1104
Gln Leu Leu His Phe His Pro His Arg Ala Ala Pro Leu Ile Ala Leu			
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Phe Gln Ser His Pro Leu Arg Thr Glu Met Pro Phe Ser Leu Tyr Phe			
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Ser Ser Pro Leu Lys Ala Pro Ala Thr Phe Ser Val Ser Ala Val Tyr			
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Thr Lys Glu Gly Ser Glu Ile Arg Asp Lys Asp Pro Ala Pro Ser Thr			
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Ser Pro Ala Phe Asp Phe Asp Gly Tyr Met Leu Arg Lys Ala Lys Ser			
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Val Asn Lys Ala Leu Glu Ala Ala Val Gln Met Lys Glu Pro Leu Lys			
100	105	110	
Ile His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val			
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Arg Pro Met Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Asp Glu			
130	135	140	
Ser Thr Ala Met Pro Ala Ala Cys Ala Val Glu Met Ile His Thr Met			
145	150	155	160
Ser Leu Met His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Leu Arg			
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Arg Gly Lys Pro Thr Asn His Met Ala Phe Gly Glu Ser Val Ala Val			
180	185	190	
Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Val Ala Ala			
195	200	205	
Ala Thr Lys Gly Ala Pro Pro Glu Arg Ile Val Arg Val Leu Gly Glu			
210	215	220	
Leu Ala Val Ser Ile Gly Ser Glu Gly Leu Val Ala Gly Gln Val Val			
225	230	235	240

Asp Val Cys Ser Glu Gly Met Ala Glu Val Gly Leu Asp His Leu Glu
245 250 255

Phe Ile His His His Lys Thr Ala Ala Leu Leu Gln Gly Ser Val Val
260 265 270

Leu Gly Ala Ile Leu Gly Gly Gly Lys Glu Glu Glu Val Ala Lys Leu
275 280 285

Arg Lys Phe Ala Asn Cys Ile Gly Leu Leu Phe Gln Val Val Asp Asp
290 295 300

Ile Leu Asp Val Thr Lys Ser Ser Lys Glu Leu Gly Lys Thr Ala Gly
305 310 315 320

Lys Asp Leu Val Ala Asp Lys Thr Thr Tyr Pro Lys Leu Ile Gly Val
325 330 335

Glu Lys Ser Lys Glu Phe Ala Asp Arg Leu Asn Arg Glu Ala Gln Glu
340 345 350

Gln Leu Leu His Phe His Pro His Arg Ala Ala Pro Leu Ile Ala Leu
355 360 365

Ala Asn Tyr Ile Ala Tyr Arg Asp Asn
370 375

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Leu Ile Gly Val Glu
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Tyr Ile Ala Tyr Arg
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Thr Ala Ala Leu Leu Thr Gly Ser Val Val Leu Gly Ala Ile Leu
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<223> PCR primer GG23F

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ctc aaa aca aga tct gat ctc agc cgt tct tct tcc gcg cgt tgc atg 98
Leu Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met
20 25 30

cca act gcc gcc gct gcc gcc ttc ccc act atc gcc acc gcc gcc caa 146
Pro Thr Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln
35 40 45

agt cag ccg tac tgg gcc gcc atc gag gcc gac ata gag aga tac ctg 194
 Ser Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu
 50 55 60

aag aaa tcc atc aca ata agg ccg ccg gag aca gtt ttc ggg ccc atg 242
Lys Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met
65 70 75

cac cac ctc acc ttc gcc gcc cca gcc acc gcc gcc tcc acc cta tgc 290
 His His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys
 80 85 90 95

ttg gcg gcg tgc gag ctc gtc ggc ggc gac cga agc caa gcc atg gca 338
Leu Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala
100 105 110

gcc gcg gcg gcg atc cat ctc gtg cac gcg gca gcc tac gtc cac gag 386
Ala Ala Ala Ala Ile His Leu Val His Ala Ala Ala Tyr Val His Glu
115 120 125

cac ctc cct cta acc gac ggg tgc agg ccc gta tcc aag ccc gca atc 434
 His Leu Pro Leu Thr Asp Gly Ser Arg Pro Val Ser Lys Pro Ala Ile
 130 135 140

cag cac aag tac ggc cgc aac gtc gag ctc ctc acc gga gac ggg att 482
Gln His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile
145 150 155

gtc ccg ttc ggg ttt gag ttg ctg gcc ggg tca gtg gac ccg gcc cga 530
Val Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg
160 165 170 175

aca gac gac ccg gat agg att ctg aga gtt ata ata gag atc agt cgg 578
Thr Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg
180 185 190

gcc ggc ggg ccg gag gga atg ata agc ggg ctg cat agg gaa gaa gaa 626
Ala Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu
195 200 205

att gtt gat gga aat acg agt tta gac ttc att gaa tat gtg tgc aag 674
Ile Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys
210 215 220

aaa aaa tac ggc gaq atg cat gct tgc ggc gcg gct tgt gga gcc ata 722

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Leu	Gly	Gly	Ala	Ala	Glu	Glu	Glu	Ile	Gln	Lys	Leu	Arg	Asn	Phe	Gly		
240					245					250					255		
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Leu	Tyr	Gln	Gly	Thr	Leu	Arg	Gly	Met	Met	Glu	Met	Lys	Asn	Ser	His		
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caa	tta	att	gat	gag	aat	ata	att	gga	aaa	ttg	aaa	gaa	ttg	gct	ctc	866	
Gln	Leu	Ile	Asp	Glu	Asn	Ile	Ile	Gly	Lys	Leu	Lys	Glu	Leu	Ala	Leu		
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gag	gag	ttg	gga	ggc	ttc	cac	ggg	aag	aac	gct	gag	ctg	atg	tcg	agc	914	
Glu	Glu	Leu	Gly	Gly	Phe	His	Gly	Lys	Asn	Ala	Glu	Leu	Met	Ser	Ser		
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ctt	gta	gcc	gag	ccg	agc	ctt	tac	gcg	gct	tagagctatt	cggtaccttc					964	
Leu	Val	Ala	Glu	Pro	Ser	Leu	Tyr	Ala	Ala								
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tttttttatta	tgaatttttt	taactgttat	tgatttcogaa	aataactgaca	atcatctaaa											1084	
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Lys	Thr	Arg	Ser	Asp	Leu	Ser	Arg	Ser	Ser	Ser	Ala	Arg	Cys	Met	Pro		
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Thr	Ala	Ala	Ala	Ala	Ala	Phe	Pro	Thr	Ile	Ala	Thr	Ala	Ala	Gln	Ser		
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Gln	Pro	Tyr	Trp	Ala	Ala	Ile	Glu	Ala	Asp	Ile	Glu	Arg	Tyr	Leu	Lys		
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Lys	Ser	Ile	Thr	Ile	Arg	Pro	Pro	Glu	Thr	Val	Phe	Gly	Pro	Met	His		
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His	Leu	Thr	Phe	Ala	Ala	Pro	Ala	Thr	Ala	Ala	Ser	Thr	Leu	Cys	Leu		
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Ala	Ala	Cys	Glu	Leu	Val	Gly	Gly	Asp	Arg	Ser	Gln	Ala	Met	Ala	Ala		
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His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Val				
145		150		160
Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Thr				
	165		170	175
Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg Ala				
	180		185	190
Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu Ile				
	195		200	205
Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys Lys				
	210		215	220
Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu				
	225		230	235
Gly Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu				
	245		250	255
Tyr Gln Gly Thr Leu Arg Gly Met Met Glu Met Lys Asn Ser His Gln				
	260		265	270
Leu Ile Asp Glu Asn Ile Ile Gly Lys Leu Lys Glu Leu Ala Leu Glu				
	275		280	285
Glu Leu Gly Gly Phe His Gly Lys Asn Ala Glu Leu Met Ser Ser Leu				
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Val Ala Glu Pro Ser Leu Tyr Ala Ala				
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<210> 13
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 1 5

<210> 14
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<220>
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oligonucleotide

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<222> (1)..(18)
<223> Forward PCR primer for cloning geranyl diphosphate
synthase large subunit wherein n at position 9 represents any nucleic
acid base

<400> 14
aarccmacna aycayatg 18

<210> 15
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
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<222> (1)..(17)
<223> Reverse PCR primer for cloning geranyl diphosphate
synthase large subunit wherein n at position 6 represents any nucleic
acid base

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